
BASE COUNT	ORIGIN
137 a	M. Fatima Bonaldo. RNA from normal foreskin melanocytes (FS37) was kindly provided by Dr. Anthony P. Albino.*
128 c	174 g
	112 t
	8 others

Query Match	77.08;	Score 219.4;	DB 24;	Length 559;
Best Local Similarity	92.08;	Pred. No. 4.3e-49;		
Matches 263;	Conservative	0;	Mismatches 19;	Indels 4;
				Gaps 3

Oy	1	gaggaaggagggaaagaaagggagaaacaaagatcttgcggtttcgttcgca	120
Db	48	GAGGGGAGGGAAGAAGGAGACAAAGATCAAGTCTCCGACGAGGTTAATAC	107
Oy	61	caagaacaatactgttcagagcgcttgagccattcatgatccctgaccttggttggcca	120
Db	108	CAGAACCATGTGTGCCACAG-GATGGCCGATTCAATGACCCTTGCGTTGTGTGGCCA	166
Oy	121	cctttgaccgcgcgcggggagacgcagccacaaccccagaggtctcccaagaacaga	180
Db	167	CCTTTGACCCGGCGCGGG--ACGCACCCACAACCCACCCGAGGTGTCCTCCAAACAGGA	224
Oy	181	gctcccaaacaaaagagcgscctgtccctgcagaaatacagcgagatccagcaactgtttg	240
Db	225	GCTCCACACAAAAGCCGCCCTGTCCCTCGAATAACGCGAATCACACACTGTTGG	284
Oy	241	tcaacgcctggcga-tgttgtgtgtgtgagtgttttgaaagtttcgaga	285
Db	285	TCAACGCTGGCATTGTGGGAGTGCGCTGTTTTCAAATTGTTTGA	330

RESULT	5
A1474188	
LOCUS	A1474188 261 bp mRNA
DEFINITION	t893d10.x1 Soares_NhhnpU_S1 Homo sapiens CDNA clone IMAGE:2115375
	3' mRNA sequence.
	EST
	30-MAR-1999

ACCESSION	A1474188	
NID	90327233	
VERSION	A1474188.1	GI:4327233
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Ekkaroyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS	Eultheria; Primates; Carnithrin; Homnidae; Homo.	
TITLE	1 (Pages 1 to 261)	
JOURNAL	NCI-GCAP http://www.ncbi.nlm.nih.gov/nci-gcap .	
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).	
	Tumor Gene Index	
	Unpublished (1997)	
	On Jun 5, 1998 this sequence version replaced gi 3188696.	

FEATURES
SOURCE

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/organism="Homo sapiens"
/dbxref="taxon:9606"
/clone_1 IMAGE:2115379.
/clone_1b =Source:NM_H19, S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NHM, pregnant uterus
2NDPU, and fetal heart 2NH15H) were mixed, and 50 circles

```

were made *in vitro*. For subtractive hybridization we used as tracer a PCR-amplified cDNA from pools of 5,000 clones. The driver was PCR-amplified cDNAs from pools of 5,000 clones. T.M.A.C.E. clones 260232-265523, 306488-345879, and 484488-489879, 1 others

[illegible]

RESULT	6
AA497118/c	
LOCUS	
DEFINITION	
AA497118.1	562 bp mRNA EST 12-AUG-1997
aa42a10.1 Soares_NhmPmu_S1 Homo sapiens cDNA clone IMAGE:823378	5
similar to SW:EST_GANGAU_P18301 SPANNINGALCIN1 PRECURSOR ; contains	
MER22.b3 MER22 repetitive element ; mRNA sequence.	

ACCESSION AA497118
 NTID 52230439
 VERSION AA497118.1 GI:2230439
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 562)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisell, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marz, M., Martin, J.,
 Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Treising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.
 TITLE WashU-Merck EST Project 1997
 COMMENT Unpublished (1997)
 On Apr 14, 1993 this sequence version replaced gi:692745.

FEATURES
Source

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/db_xref="taxon:9606"
/clone IMAGE:823578
/clone_1lib="Soares_NHMPU_S1"
/tissue_type="Pooled human melanocyte, fetal heart,
pregnant uterus"

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="male"
/dev_stage="adult"
/tissue_type="blood"

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COMMENT	FEATURES	SOURCE	BASE COUNT	ORIGIN
ASAH1 CHEM IND CO LTD				
OS Alcaligenes sp.				
PN JP 1993161492-A/1				
PD 29-JUN-1993				
PF 08-JUN-1991 JP 1991193471				
PI HORIIYU KAZUO, TAKAHASHI MANOBU, MIZOGUCHI JUNZO, PI				
IMAMURA SHIGETUKI				
PC C12N1/21.C12N9/04.C12N15/53.(C12N9/04.C12N1.19).C12N15/53.				
C12N1.05);				
CC strandedness: Double;				
CC topology: Linear;				
CC hypothetical: No;				
CC anti-sense: No;				
CC *source: strain-No.921;				
CC *source: deposit-FERM BP-2570;				
CC *source: clone-pcch2;				
FF key				
FF Location/Qualifiers				
FF CDS				
FT 416..1381				
FT /product="recombinant carnitine				
FT FT				
FT dehydrogenase'				
FT /note="recombinant CDH"				
FT 416..1378				
FT /product="recombinant carnitine				
FT FT				
FT mat_peptide				
FT dehydrogenase'				
FT Location/Qualifiers				
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FT /organism="Alcaligenes sp."				
FT /db_xref="taxon:518"				
FT 290 a 536 c 477 g 237 t				

54: em_est22:*
 55: em_est23:*
 56: em_est24:*
 57: em_est25:*
 58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	257	100.0	625	29	AA195455	AA195455 z136n08.r
2	233	90.7	562	34	AA457118	AA457118 aa42a10.r
3	229.4	89.3	530	34	AA456244	AA456244 z136n08.r
4	174	67.7	308	31	AA298636	AA298636 EST114243
5	166	64.6	480	42	AI087984	AI087984 co24f09.x
6	154.8	60.2	546	48	AI549761	AI549761 ve76f01.y
7	142	55.3	486	34	AA497040	AA497040 aa42a10.s
8	120.2	46.8	507	33	AA423593	AA423593 ve76f01.r
9	109.8	42.7	465	30	AA223369	AA223369 z108d07.r
10	79.6	31.0	559	24	H98185	H98185 yx08b10.s1
11	79	30.7	739	42	AI115911	AI115911 ue96d11.y
12	69.6	27.1	455	42	AI086972	AI086972 oz64f10.x
13	58.2	22.6	301	31	AA297962	AA297962 EST113548
14	50	19.5	366	22	R73246	R73246 y109f01.r1
15	49	19.1	483	22	R72337	R72337 y188d08.r1
16	48	18.7	412	22	R48681	R48681 y165d07.r1
17	33.2	12.9	367	20	DA0566	DA0566 RICS2631A R
18	33.2	12.9	644	43	AU030960	AU030960 AU030960
19	33.2	12.9	759	43	C99305	C99305 C99305 Rice
20	33.2	12.9	735	51	AU068621	AU068621 AU068621
21	33.2	12.9	845	51	AU068622	AU068622 AU068622
22	32.8	12.8	460	22	R55634	R55634 y177e10.r1
23	32.8	12.8	547	26	W97849	W97849 m905h07.r1
24	32.8	12.8	449	29	AA155095	AA155095 mr24h09.r
25	32.8	12.8	600	30	AA204544	AA204544 mu66y09.r
26	32.8	12.8	529	33	AA414468	AA414468 vc59b09.s
27	32.8	12.8	450	44	AI322715	AI322715 mr24h09.y
28	32.8	12.8	545	44	AU043089	AU043089 AU043089
29	32.6	12.7	442	49	AU055934	AU055934 AU055934
30	32.6	12.7	721	49	AU056229	AU056229 AU056229
31	32.2	12.5	396	20	DA1073	DA1073 RICS3338A R
32	32.2	12.5	631	38	AA792592	AA792592 v888f01.r
33	31.4	12.2	513	45	AA859654	AA859654 UI-R-EO-b
34	31.2	12.1	490	27	AA030801	AA030801 m127b12.r
35	30.8	12.0	264	39	AA849176	AA849176 EST191943
36	30.8	12.0	247	51	AI710086	AI710086 UI-R-AA1-
37	30.8	12.0	411	51	AI710973	AI710973 UI-R-AE1-
38	30.4	11.8	440	28	C20066	C20066 C20066 Rice
39	30.2	11.8	365	42	AI153589	AI153589 vz89b04.r
40	30.2	11.8	458	48	AI608090	AI608090 va09a02.y
41	30.2	11.8	613	50	AI665869	AI665869 606003A01
42	30.2	11.8	579	50	AI666172	AI666172 606005G11
43	30.2	11.8	590	50	AI667796	AI667796 605028B02
44	30.2	11.8	586	50	AI677120	AI677120 605050A05
45	30.2	11.8	519	51	AI737845	AI737845 606042D11

ALIGNMENTS

RESULT 1
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 LOCUS
 DEFINITION z136n08.r1 Soares_NhmPv_S1 Homo sapiens CDNA clone IMAGE:665535 5' similar to SW:CSRP_ANGAD P18301 STANNIOCALCIN PRECURSOR ; mRNA
 ACCESSION AA195455
 NID 91785219

VERSION AA195455.1 GI:1785219
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 625)
 Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 On Sep 12, 1996 this sequence version replaced gi:1290840.

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 463.

FEATURES
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 1..625
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 /db_xref="taxon:9606"
 /map="959002:1:1q23.3-1q25.3"
 /clone="IMAGE:665535"
 /clone.lib="Soares_NHMPU_S1"
 /tissue.type="Pooled human melanocyte, fetal heart, and
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 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT7T3D-Pac
 (Pharmacia) with a modified polylinker; Site:1: Not I;
 Site:2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus
 NBHPU, and fetal heart NBH19M) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 127 a 175 c 171 g 145 t 7 others

BASE COUNT
 127 a 175 c 171 g 145 t 7 others

Query Match 100.0%; Score 257; DB 29; Length 625;
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 gttgaatgttcgagaaacactctgtgagatcggggtcacaatgagattgcatgac 60
 Db 470 gttgaatgttcgagaaacactctgtgagatcggggtcacaatgagattgcatgac 411
 Oy 61 tttctgcacaaagctggaataattgagccagggcaagtcattcaacaagagcctt 120
 Db 410 tttctgcacaaagctggaataattgagccagggcaagtcattcaacaagagcctt 351
 Oy 121 gaaatgaaagccagctctgagccagagttcgggtgataagccgagagtgccgcgc 180
 Db 350 gaaatgaaagccagctctgagccagagttcgggtgataagccgagagtgccgcgc 291
 Oy 181 catagaggaatgtgtccaggttgcagcggaatgtactcaagcagcactgtgagc 240
 Db 290 catagaggaatgtgtgtccaggttgcagcggaatgtactcaagcagcactgtgagc 231
 agctgcacagagagaca 257

Db 230 GCGTCCAGAGAGACA 214

RESULT 2
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 LOCUS
 DEFINITION
 aa497118.1 562 bp mRNA EST 12-AUG-1997
 aa42a10.f1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:823578 5'
 similar to SW:GSTP_PANAU_P18301 STANNOCALCIN PRECURSOR; contains
 MER22.b3 MER22 repetitive element; mRNA sequence.

ACCESSION
 AA497118
 NID
 G2230439
 VERSION
 AA497118.1 GI:2230439

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 562)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schellendberg, K., Stepien, M., Tan, F., Thelasing, B.,
 White, Y., Wylie, T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished (1997)
 On Apr 14, 1993 this sequence version replaced gi:692745.

TITLE
 JOURNAL
 COMMENT

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 497.

FEATURES
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 /clone.lib="Soares_NHMPU_S1"
 /tissue.type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT7T3D-Pac
 (Pharmacia) with a modified polylinker; Site:1: Not I;
 Site:2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus
 NBHPU, and fetal heart NBH19M) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT
 118 a 165 c 152 g 126 t 1 others

Query Match 90.7%; Score 233; DB 34; Length 562;
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 Matches 255; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Oy 1 gttgaatgttcgagaaacactctgtgagatcggggtcacaatgagattgcatgac 60
 Db 460 gttgaatgttcgagaaacactctgtgagatcggggtcacaatgagattgcatgac 401
 Oy 61 tttctgcacaaagctggaataattgagccagggcaagtcattcaacaagagcctt 120
 Db 400 tttctgcacaaagctggaataattgagccagggcaagtcattcaacaagagcctt 342

121 gaatgaagcagcagctctgagcagaggttcgctgcatagccggaagtcggc 180
 341 GAATTAAGGCCAC -CTTCGGCAGAGTTCGGCTGATAGCCGAGTGGCCGC 283
 181 catcaggaagatggtctccagttgagcaggaatgctactcaagcagacgtgtgc 240
 282 CATCAGGGAATGTGTCTCCAGTTCAGCGGAATGCTACTCAAGCAGACGCTGTGCGC 223
 241 ggcctccagcagagaca 257
 222 GCGTCCAGGAGACA 206

RESULT 3 530 bp mRNA EST 06-JUN-1997
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 LOCUS 2x99c03.r1 Soares.NhMpu.Homo sapiens CDNA clone IMAGE:811876 5'
 DEFINITION Similar to TR:G975298 STANNIOCALCIN PRECURSOR. ; mRNA
 sequence.

ACCESSION AA56244 GI:2279454
 NID 92179454
 VERSION AA56244.1 GI:2279454
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Metazoa; Catarrhini; Homiidae; Homo.
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 530)
 Hillier, L., Allen, M., Bowles, J., Dubuque, T., Gelsel, G., Jost, S.,
 Knapp, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 McEwen, B., Schellenberg, K., Stepien, M., Tan, F., Theisberg, B.,
 White, I., Wyllie, T., Waterston, R., and Wilson, R.
 Whitehead EST Project 1997

TITLE Unpublished (1997)
 JOURNAL On Jan 25, 1995 this sequence version replaced gi:637783.
 COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1817
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through JNLT; contact the
 IMAGE Consortium (info@image.lln.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer -28m13 rev2 ET from Amersham
 High quality sequence stop: 421.
 Location/Qualifiers

FEATURES

source

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 /clone_id="Soares.NhMpu.S1"
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 /lab_host="DH10B"
 /note="Organ: mixed (see below). Vector: pTZ19-Pac
 (Pharmacia) with a modified polylinker site. 1: Not I;
 Site 2: Eco RI. Equal amounts of plasmid DNA from three
 normalised libraries (melanocyte 2NDH, pregnant uterus
 NBH19, and fetal heart NBH19) were mixed and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as target in a sub-tractive hybridization
 reaction. The driver was pc-ampified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of 1 M.A.G.E. clones 260232-265223,
 340488-345479, and 484480-489479.
 115 a 160 c 138 g 117 t

BASE COUNT

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 Best Local Similarity 98.48; Pred. No. 2.1e-63;
 Matches 253; Conservatively 0; Mismatches 1; Indels 3; Gaps 2;
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 455 GTTTGAATTTTCGAGAACCACTCTTGAGATTGCGGCTTCATATGGATTTCATGAC 396
 61 ttttcacacagctgtgaaatttgatccagcagcagtccttcattcaagaagcgcct 120
 395 TTTTCGACACAGCTGTGAAATTTGAT -CCAGGCGAAGTCATTCATCAAGACGCCCT 337
 121 gaatgaagcagcagcagctctgagcagagtttcgctgacatgaagcagagtcggc 180
 336 GAATGAAGGCCCA -CTTCGGCAGAGTTCGGCTGATATGACCGAAGTGGCCGC 279
 181 catcaggaagatggtctccagttgagcaggaatgctactcaagcagacgtgtgc 240
 278 CATCAGGGAATGTGTCTCCAGTTCAGCGGAATGCTACTCAAGCAGACGCTGTGCGC 219
 241 ggcctccagcagagaca 267
 218 GCGTCCAGGAGACA 202

RESULT 4 308 bp mRNA EST 18-APR-1997
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 LOCUS EST114243 HSC172 cells II Homo sapiens CDNA 5' end similar to
 DEFINITION similar to conspicles of stannius protein, mRNA sequence.
 ACCESSION AA298636
 NID 91950968
 VERSION AA298636.1 GI:1950968
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Metazoa; Catarrhini; Homiidae; Homo.
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 308)
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weissbrock, K.G., Gockayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Val, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, N.S.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S.,
 Glodet, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.D., Sauder, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
 Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, G.A.,
 Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Frazer, C.M., and Venter, J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 85 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 On Sep 12, 1996 this sequence version replaced gi:1392816.
 Other ESTs: TRC192796
 Contact: Kerlavage, AR
 Bioinformatics for Genomic Research
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/ngl/ngl.html>)

TITLE
 JOURNAL MEDLINE
 COMMENT

10

GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: November 19, 1999, 05:17:41; Search time 1904.28 Seconds
(without alignments)
271.391 Million cell updates/sec

Title: US-09-193-881-7

Sequence: 1 gtagagatgagagaccctcggg.....cagcagcctctgtgtcttca 262

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database:

EST.*
1: em_est1.*
2: em_est2.*
3: em_est3.*
4: em_est4.*
5: em_est5.*
6: em_est6.*
7: em_est7.*
8: em_est8.*
9: em_est9.*
10: em_est10.*
11: em_est11.*
12: em_est12.*
13: em_est13.*
14: em_est14.*
15: em_est15.*
16: em_est16.*
17: em_est17.*
18: em_est18.*
19: em_est19.*
20: em_est20.*
21: em_est21.*
22: em_est22.*
23: em_est23.*
24: em_est24.*
25: em_est25.*
26: em_est26.*
27: em_est27.*
28: em_est28.*
29: em_est29.*
30: em_est30.*
31: em_est31.*
32: em_est32.*
33: em_est33.*
34: em_est34.*
35: em_est35.*
36: em_est36.*
37: em_est37.*
38: em_est38.*
39: em_est39.*
40: em_est40.*
41: em_est41.*
42: em_est42.*
43: em_est43.*
44: em_est44.*
45: em_est45.*
46: em_est46.*
47: em_est47.*
48: em_est48.*
49: em_est49.*
50: em_est50.*
51: em_est51.*
52: em_est52.*
53: em_est53.*

54: em_est22.*
55: em_est23.*
56: em_est24.*
57: em_est25.*
58: em_est26.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	150	57.3	277	34	AA63548	AA63548 zx72c07.r
2	109	41.6	426	39	AA825343	AA825343 oe63d02.s
3	94.2	36.0	434	37	AA704088	AA704088 ag47d04.s
4	65.6	28.0	506	26	W46285	W46285 zc31a07.s1
5	50	19.1	493	30	AA223294	AA223294 zx72c07.s
6	41	15.6	413	34	AA463501	AA463501 zx72c07.s
7	35.2	13.4	371	44	AI301775	AI301775 qn08c09.x
8	34.6	13.2	481	42	AI131393	AI131393 qcl1d04.x
9	34.6	13.2	532	43	AI193018	AI193018 qe69a11.x
10	34.6	13.2	439	44	AI291401	AI291401 qm84b06.x
11	34.6	13.2	457	44	AI298949	AI298949 qn01b05.x
12	34.6	13.2	205	45	AI335422	AI335422 lb66c04.x
13	34.6	13.2	460	45	AI365683	AI365683 mo90h07.x
14	34.6	13.2	457	45	AI378452	AI378452 lc79d05.x
15	34.6	13.2	379	46	AI45370	AI45370 lk02d09.x
16	34.6	13.2	516	46	AI459079	AI459079 lk02d09.x
17	34.6	13.2	397	47	AI498632	AI498632 tm47d07.x
18	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
19	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
20	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
21	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
22	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
23	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
24	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
25	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
26	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
27	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
28	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
29	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
30	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
31	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
32	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
33	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
34	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
35	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
36	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
37	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
38	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
39	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
40	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
41	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
42	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
43	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
44	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x
45	34.6	13.2	516	47	AI498632	AI498632 tm47d07.x

ALIGNMENTS

RESULT 1
AA63548 277 bp mRNA EST 10-JUN-1997
LOCUS zx72c07.r1 Soares total fetus NB2HF8_9w Homo sapiens cDNA clone
DEFINITION IMAGE:797004 5' mRNA sequence.
ACCESSION AA63548
NID 92188432
VERSION AA63548.1 GI:2188432

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 277)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucuba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT On May 8, 1995 this sequence version replaced g1:800889.

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 266.

FEATURES**source****location/Qualifiers**

1. 277
 /organism="Homo sapiens"
 /db_xref="GDB:6041749"
 /db_xref="taxon:9606"
 /clone="IMAGE:797004"
 /clone.lib="Soares.total_fetus_Nb2HF8_9w"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGGCGCGCTTAATTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

53 a 64 c 104 g 56 t

Query Match 57.3%; Score 150; DB 34; Length 277;
Best Local Similarity 98.4%; Pred. No. 8.5e-29;

Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

74 gagggcgccggcgtatccctgacccctgtctcttcacatcgtgagtcagtggtg 133
 |||||
 Db 2 GAGGCGCCGCCCTTACCTCTGCTGCTTCTTCATCTGTGAGTCACTGCTG 61
 |||||
 Oy 134 tcggcgctcgt 193
 |||||
 Db 62 TCGGCGCTCTGT 120
 |||||
 Oy 194 gagctggcaccacagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 253
 |||||
 Db 121 GAGCTGGG-CACACAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 178
 |||||
 Oy 254 ggtgtct 259
 |||||
 Db 179 GGTGCT 184

RESULT 2
 3343 AA825343 426 bp mRNA EST 24-FEB-1998
 0e63602.81 NCI-CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416291 3',
 RNA sequence

ACCESSION AA825343
NID 02898646
VERSION AA825343.1 GI:2898646
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 426)
 NCI-CGAP/ftp://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1995 this sequence version replaced g1:814172.

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 www.bic.llnl.gov/db/ftp/image/image.html

FEATURES**source****location/Qualifiers**

Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 409.
 1. 426
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1416291"
 /clone.lib="NCI-CGAP_Lu5"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: Lung; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker. 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

84 a 81 c 162 g 99 t

Query Match 41.6%; Score 109; DB 34; Length 426;
Best Local Similarity 97.9%; Pred. No. 2.2e-76;

Matches 142; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Oy 115 tcctgtgagtcagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 174
 |||||
 Db 1 TCTGTGAGTCACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 80
 |||||
 Oy 175 tggcaggcaggcggcccgaggcaggcaggcaggcaggcaggcaggcaggcaggc 234
 |||||
 Db 61 GAGCAGGCGAGGG-CGCCGAGCTGGGCCACACAGT-GGTCTGGGCTCG-CACGAAGC 117
 |||||
 Oy 235 ttcctgtgacagcagcctcgtgtgtct 269
 |||||
 Db 118 TCTCTGTGACAGCAGCCTTGTGCTGCT 142

RESULT 3
 3343 AA704088 334 bp mRNA EST 12-MAY-1999
 4947404.11 J1a bone marrow stroma Homo sapiens cDNA clone
 IMAGE:1119943 3', mRNA sequence.
 AA704088
 NID 92714006

Query Map: 54.4%; Score 163.6; DB 49; Length 282;
 Best Local Similarity 85.3%; Pred. No. 4.1e-38;
 Matches 192; Conservative 32; Indels 1; Caps 1;

1 agaaccaagctctccagggcccaacagggagagagacatcctccagagccagc 60
 165 AGGCTCAGCTCTCCAGGCTCCACACGAGACACACACCTACTTAAAG----- 217
 61 agtagagagctccagaggtcccaaggtgagcagaggtgagcagagcacaacagct 120
 217 -----CCATACAGGTGCCAAGGTGAGCGAGGAGCAAAAGCCAGCAATGCC 266
 121 cagccagagagagagagcagggaggtgaggtccagagagctccagagagagagtg 80
 267 CATCTGAGGAGCAGACAGCGGCGCCAGAGCGCTCAGGAGCCCTTGGAGAGTGAAGTGG 326
 181 gaagagagagagagagaggtgaggttccgagagagagagagagagagagagagag 240
 327 GAGATGACACAGTGTGATATCCGATATCCGAGATCCGAGGAGCAATGAAAACCGGCGCATGAA 385
 241 attctccacagcgcgtccatctctctatctatgagacattcaaacacattacatta 299
 386 AGCTTCTCCAGGCTGTCATTTCTATCTATGACATTCACAAACATTTTACATTAA 444

AA373922 4
 LOCUS 243 bp mRNA EST 21-Apr-1997
 DEFINITION AA373922 HSC172 cells 1 Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA373922
 NID 92026242
 VERSION AA373922.1 GI:2026242
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homini; Hominidae; Homo.
 1 (bases 1 to 243)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulmer,R.A.,
 Buit,C.J., Lee,N.H., Kirkness,E.F., Weissstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fitchman,J.L., Geoghegan,N.S.,
 Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., J.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marnaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,K., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Ceol,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Danke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.M., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 On May 5, 1995 this sequence version replaced g1:798247.

RESULT 3
 LOCUS AV001175 281 bp mRNA EST 26-May-1999
 DEFINITION AV001175 Mus musculus C57BL/6J kidney Mus musculus cDNA clone
 0610011D11 mRNA sequence.
 ACCESSION AV001175
 NID 94778025
 VERSION AV001175.1 GI:4778025
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 282)
 Carninci,P., Shibata,K., Ozawa,Y., Honno,H., Ito,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
 Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
 Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Natsuna,H., Oda,H.,
 Owa,K., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sobabe,Y.,
 Sugahara,Y., Suzuki,H., Suzuki,M., Tachino,M., Tomaru,Y.,
 Tomioka,M., Watanabe,S., Yagane,M., Yamamura,T., Yokota,T.,
 Yoshino,M., Yamatsuta,M., Okazaki,Y. and Hayashizaki,Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 On Jun 5, 1998 this sequence version replaced g1:3188847.

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 On May 5, 1995 this sequence version replaced g1:798247.

CONTACT: Kerlavage, AR
 Bioinformatics for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (http://www.tigr.org/tdb/hgi/hgi.html)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..243
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):178301"

FEATURES
 Source
 1..282
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="0610011D11"
 /clone_1lb="Mus musculus C57BL/6J kidney"
 /clone_type="kidney"
 /clone_type="kidney"
 79 a 69 c 78 g 49 t 7 others

BASE COUNT
 ORIGIN

```

OligoName: "ras_40090"
/db_xref: taccn:106435
/clone_id: "106435"
/clone_id: "106435" (different stromal cell line MRLR8)
/cell_line: "2103" (undifferentiated)
/cell_host: "2103"
/notes: Vector: p773D-Pac (Pharmacia) with a modified
polylinker. Site_1: EcoRI, Site_2: NotI, 1st strand cDNA

```

Contact: Maria M/WashU-NCI House Est Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501 St. Louis MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:600847
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end

Accession # AA126174

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 251)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,
Chiswick, S., Dietrich, N., Dubuque, T., Favell, A., Gibb, W.,
Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L.,
Roeding, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J.,
Tevaak, E., Underwood, P., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT On Sep 12, 1996 this sequence version replaced g1:1402309.

CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: eastw@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 349 Std Error: 0.00
Seq primer: -40M13 fwd from Amersham.
Location/Qualifiers

FEATURES
SOURCE
1. 251
/organism="Homo sapiens"
/db_xref="GDB:4594021"
/db_xref="taxon:9606"
/clone="IMAGE:564957"
/clone_id="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: Lung; Vector: pBluescript SK-; Site: 1:
EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Small cell carcinoma cell line NCI-H69. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'."
BASE COUNT 87 a 62 c 47 g 55 t
ORIGIN

Query Match 100.0%; Score 247; DB 29; Length 251;
Best Local Similarity 100.0%; Pred. No. 4, 1e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 gttgaagcattatctgacagatagatagataactgataaataaataaag 60
D 1 GTTGAAGCATTATTATGATGACAGATATGTAGATATACGATTAATAAAG 60
Y tgaatcgagatttgaagcagtggttataataactatagggccactccctggac 120
D 61 TGAATCGAGATTGAAAGCAGTGTATAAATACTCATAGGGCCACTCCCTGGAC 120
Y agtgcaccccccagcagacagatgctcagaatactacatagaaatgacac 180
D 121 AGTGCACCCCCAGCAGACAGATGCTCAGAAATTAACATAGAAATGACACTC 180
Y ctccctcacccctgccaagagctctgaacgcgaagcccccacaagaactgaat 240
D 181 CTCCTCACCCCTGCGCAAGAGCTCTGACCGCAGGCCCCACACAAGAAATG 240
241 agttgg 247
AGTTGG 247

RESULT 2
LOCUS A1400098 380 bp mRNA EST 30-MAR-1999
DEFINITION t62a09.x1 Soares NSF_F8_9W OT_PA_P_S1 Homo sapiens CDNA clone
IMAGE:211336 3', mRNA sequence
ACCESSION A1400098
NID 94243185
VERSION 1 GI:4243185
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 380)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncic99/
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Mar 20, 1998 this sequence version replaced g1:2980279.

CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 379 Std Error: 0.00
Seq primer: -400P from Glyco
High quality sequence stop: 379.
Location/Qualifiers

FEATURES
SOURCE
1. 380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p11.04:18q13.2"
/clone="IMAGE:211336"
/clone_id="SOARES_NSF_F8_9W OT_PA_P_S1"
/lab_host="TDH10B"
/note="Organ: pooled; Vector: pT73D-Pac (pharmacia) with
a modified polylinker; Site: 1: Not I; Site: 2: EcoRI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NDHF pool 1:
309384-510919, 343208-325885 Soares NDHF pool 1:
145932-148335, 147720-148101, 148872-149255, 15002 -
150407, 151176-152327 Soares NDHF pool 1:
756280-760583, 778104-774407 Soares NDHF pool 1:
704776-306311, 360136-322823, 826280-326663 Soares NDHF
pool 1: 723720-726407, 735080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 105 a 96 c 97 g 82 t
ORIGIN

Query Match 100.0%; Score 247; DB 46; Length 380;
Best Local Similarity 100.0%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 gttgaagcattatctgacagatctgagataactgataaataaataaag 60
D 61 GTTGAAGCATTATTATGATGACAGATATGTAGATATACGATTAATAAAG 65
Y tgaatcgagatttgaagcagtggttataataactatagggccactccctggac 120
D 66 TGAATCGAGATTGAAAGCAGTGTATAAATACTCATAGGGCCACTCCCTGGAC 125
Y agtgcaccccccagcagacagatgctcagaatactacatagaaatgacac 180
D 121 AGTGCACCCCCAGCAGACAGATGCTCAGAAATTAACATAGAAATGACACTC 185
126 AGTGCACCCCCAGCAGACAGATGCTCAGAAATTAACATAGAAATGACACTC 185

QY 241 ct 242
Db 143 CT 142

RESULT 3
AA704088 434 bp mRNA EST 12-MAY-1999
LOCUS ag47d04.1 via bone marrow stroma Homo sapiens CDNA clone
DEFINITION IMAGE:111943.3', mRNA sequence.

ACCESSION AA704088
NID 92714006
VERSION AA704088.1 GI:2114006

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 434)

REFERENCE Jia, J., Rodey, P., Leung, M., Schuster, G., Powell, J., Yang, L.,
Legion, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T.,
Maire, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y.,
Wille, T., Wagerston, R., Wilson, R. and Francomano, C.
WASHU-MGB/MHGR EST Project

TITLE WASHU-MGB/MHGR EST Project
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1400964.

CONTACT: Wilson RK, Jia L
WASHU-MGB/MHGR EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd ET from Amersham
High quality sequence stop: 434

FEATURES

source
1..434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:111943"
/clone_lib="via bone marrow stroma"
/sex="mixed"
/tissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XLI-blue MRF/SOLR"
/note="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;
mRNA made from human bone marrow stroma. CDNA made by
oligo-dt priming. Directionally cloned. Size selected for
average insert size 50.5 kb. Library supplied by Dr. Labin
Jia (NHGR)."

BASE COUNT

117 a 141 c 88 g 93 t

Query Match 92.3%; Score 223.4; DB 37; Length 434;
Best Local Similarity 97.1%; Pred. No. 1e-56;
Matches 235; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 ggaagctctggtctgtctccgcggaagtcagggcgctgattcaggaagcagagagtaaa 60
DB 350 GCAGCCTCGTGTCTCCCGGCAAGTCAGGCGCTGATTCAGACAGAGTGA 291
QY 61 ttttaaaataatcctgtctgagtcagggananggtgtggagagagcagggccgag 120
DB 290 TGTAAATAATATTCCTTGAAGACAGGAAAGCGTGAAGAGGAGGAGGCGCCAGG 231
QY 121 ggggtgtgtgtcgaactgaattcattctgtgtgggcttgcgttcagagctc 180
DB 230 GGGTGTGTGTGTCGCAACATCAATTCATTCTGTGT- GGGACTTGGCGTTCAGAGCTC 172

QY 181-ctggcagangntggagggagagtcattctcattgtgaattctgaagccattgactct 240
DB 171 TTGGCAGGGGTGAGGAGAGAGTCTCTATGTGTAATTTCTGACCATTTGACTGT 112

QY 241 ct 242
Db 111 CT 110

RESULT 4
AA223294 493 bp mRNA EST 11-MAR-1998
LOCUS z708d07.s1 STRA gene NT2 neuronal precursor 937230 Homo sapiens
DEFINITION CDNA clone IMAGE:650895.3', mRNA sequence.

ACCESSION AA223294
NID 9243818
VERSION AA223294.1 GI:1943818

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 493)

REFERENCE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, S.,
Kucaba, T., Lacy, M., Lennon, G., Maire, M.,
Krizman, D., Moore, B., Schellenger, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wille, T., Wagerston, R. and Wilson, R.
WASHU-MGB/MHGR EST Project

TITLE WASHU-MGB/MHGR EST Project
JOURNAL Unpublished (1997)
COMMENT On May 8, 1995 this sequence version replaced gi:801470.

CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1907 Std Error: 0.00
Seq primer: 41m13 fwd. ET from Amersham
High quality sequence stop: 354

FEATURES

source
1..493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:650893"
/clone_lib="STRAGEN NT2 neuronal precursor 937230"
/dev_stage="neuroepithelial cells"
/tissue_type="neuroepithelial cells"
/note="Organ: brain; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
oligo dt. Undiluted, exponentially growing neuroepithelial
cells (NTera-2/cl.D). Average insert size: 1.0 kb.
Uni-ZAP XR Vector. 5' adaptor sequence: 5' GAATTCGCGACGAG
3' -3' adaptor sequence: 5' CTCGACTTTTCTTTTCTTTT 3'."

BASE COUNT

128 a 146 c 99 g 117 t

Query Match 88.4%; Score 214; DB 30; Length 493;
Best Local Similarity 97.1%; Pred. No. 6.7e-54;
Matches 236; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 ggaagctctggtctgtctccgcggaagtcagggcgctgattcaggaagcagagagtaaa 59
DB 388 GCAGCCTCGTGTCTCCCGGCAAGTCAGGCGCTGATTCAGACAGAGTGA 329
QY 60 atgtaaaaataatcctgtctgagtcagggananggtgtggagagagcagggcgag 119

1

LOCUS 292 bp mRNA EST 11-DEC-1995
DEFINITION y00108.t1 Soares melanocyte 2NBHM Homo sapiens CDNA clone
MAG251007.5, mRNA sequence
ACCESSION H97088
H97088 91114131
VERSION H97088.1 GI:1114131
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 292)
Hillier, L., Clark, N., Dubuque, T., Ellistop, K., Hawkins, M.,
Holman, N., Hiltman, M., Kucaba, T., Le, M., Lennon, G., Maize, M.,
Parsons, J., Rifkin, L., Rohlfs, J., Soares, M., Tan, P.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Wash-Merck EST Project
Unpublished (1995)
COMMENT On May 8 1995 this sequence version replaced gi:789459.
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108.
Tel: 314.286 1800
Fax: 314.286 1810
Email: eseev@wustl.edu
High quality sequence stops: 262
Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (lmln@image.jlni.gov) for further information.
Insert Length: 1051 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 262.
Location/Qualifiers
1..292
/organism="Homo sapiens"
/db_xref="GB:3868713"
/db_xref="cdon:9605"
/clone="IMAGE:251007"
/clone_1kb="Soares melanocyte 2NBHM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pUT7D (pharmacia) with a modified
polymerase. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA"

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/organism="Homo sapiens"
/db_xref="GDB:1255485"
/db_xref="taxon:9606"
/clone_image="IMAGE:323973"
/clone_lib="Scarsenescant_fibroblasts_NDHS"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT73D (Pharmacia) with a modified

```

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/organism="Homo sapiens"
/seq_xref="taxon:9606"
/map="19p12.00;19q13.2"
/clone_image="21/3336"
/clone_lib="Scayes_NSF_F8_9W_OF_PA_P_S1"
/lab_host="DH10b"
/notes="Organ: pooled; Vector: pRTT3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP polymerization, this DNA was used as target in
a subtractive hybridization reaction. The driver was

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